SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) **Designated States** *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

SEQUENCE LISTING

<110> Imperial College Innovations LTD
Oregon Health and Science University

<120> Modification of Feeding Behavior

<130> 9248 WO/JSvn

<150> GB 02 00507.2
<151> 10-01-2002

<150> PCT/US02/31944
<151> 24-09-2002

<160> 341

<170> PatentIn version 3.1

<210> 1
<211> 36
<212> PRT
<213> Homo sapiens

<400> 1

Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 2
<211> 36
<212> PRT
<213> Homo sapiens

<400> 2

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 3
<211> 36
<212> PRT
<213> Homo sapiens

<400> 3

Ala Ser Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr

35

<210> 4
<211> 3
<212> PRT
<213> Homo sapiens

<400> 4

000
1

<210> 5
<211> 36
<212> PRT
<213> Rattus sp.

<400> 5

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 6
<211> 36
<212> PRT
<213> Sus sp.

<400> 6

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 7
<211> 36
<212> PRT
<213> Cavia porcellus

<400> 7

Tyr Pro Ser Lys Pro Glu Ala Pro Gly Ser Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ala Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 8
<211> 36
<212> PRT
<213> Rana sp.

<400> 8

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Met Thr Lys Tyr Leu Thr Ala Leu Arg His Tyr Ile Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 9
<211> 36
<212> PRT
<213> Raja sp.

<400> 9

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Asp Asp Ala Ala Pro Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 10
<211> 36
<212> PRT
<213> Dogfish sp.

<400> 10

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Pro Pro Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 11
<211> 36
<212> PRT
<213> Lampetra sp.

<400> 11

Phe Pro Pro Lys Pro Asp Asn Pro Gly Asp Asn Ala Ser Pro Glu Gln
1 5 10 15

Met Ala Arg Tyr Lys Ala Ala Val Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 12
<211> 36
<212> PRT
<213> Petromyzontidae gen. sp.

<400> 12

Met Pro Pro Lys Pro Asp Asn Pro Ser Pro Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Lys Tyr Met Leu Ala Val Arg Asn Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 13
<211> 36
<212> PRT
<213> Rattus sp.

<400> 13

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 14
<211> 36
<212> PRT
<213> Oryctolagus cuniculus

<400> 14

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 15
<211> 36
<212> PRT
<213> Canis familiaris

<400> 15

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 16
<211> 36
<212> PRT
<213> Sus sp.

<400> 16

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 17
<211> 36
<212> PRT
<213> Bos taurus

<400> 17

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 18
<211> 36
<212> PRT
<213> Ovis aries

<400> 18

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Asp Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 19
<211> 36
<212> PRT
<213> Cavia porcellus

<400> 19

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 20
<211> 36
<212> PRT
<213> Avian

<400> 20

Tyr Pro Ser Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp

1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 21
<211> 36
<212> PRT
<213> Rana sp.

<400> 21

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 22
<211> 36
<212> PRT
<213> Carassius auratus

<400> 22

Tyr Pro Thr Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 23
<211> 36
<212> PRT
<213> Dogfish sp.

<400> 23

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 24
<211> 36
<212> PRT
<213> Lampetra sp.

<400> 24

Pro Pro Asn Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Leu Ser Ala Val Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 25
<211> 36
<212> PRT
<213> Ovis aries

<400> 25

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 26
<211> 36
<212> PRT
<213> Sus sp.

<400> 26

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 27
<211> 36
<212> PRT
<213> Canis familiaris

<400> 27

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 28
<211> 36
<212> PRT
<213> Felis catus

<400> 28

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 29
<211> 36
<212> PRT
<213> Bos taurus

<400> 29

Ala Pro Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 30
<211> 36
<212> PRT
<213> Rattus sp.

<400> 30

Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr His Glu Gln
1 5 10 15

Arg Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 31
<211> 36
<212> PRT
<213> Mus musculus

<400> 31

Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 32
<211> 37
<212> PRT
<213> Cavia porcellus

<400> 32

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Gln Met Ala Gln Tyr Ala Ala Glu Met Arg Arg Tyr Ile Asn Met Leu

20 25 30

Thr Arg Pro Arg Tyr
35

<210> 33
<211> 36
<212> PRT
<213> Gallus gallus

<400> 33

Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Glu Asp
1 5 10 15

Leu Ile Arg Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg His Arg Tyr
35

<210> 34
<211> 36
<212> PRT
<213> Alligator sp.

<400> 34

Thr Pro Leu Gln Pro Lys Tyr Pro Gly Asp Gly Ala Pro Val Glu Asp
1 5 10 15

Leu Ile Gln Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg Pro Arg Phe
35

<210> 35
<211> 36
<212> PRT
<213> Rana catesbeiana

<400> 35

Ala Pro Ser Glu Pro His His Pro Gly Asp Gln Ala Thr Pro Asp Gln
1 5 10 15

Leu Ala Gln Tyr Tyr Ser Asp Leu Tyr Gln Tyr Ile Thr Phe Ile Thr
20 25 30

Arg Pro Arg Phe
35

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 36

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 37
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 37

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 38
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 38

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 39
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 39

Arg His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 40
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 40

Arg His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 41
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 41
Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 42

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 43
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 43

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 44

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 45

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 46
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 46

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr

1 5 10

<210> 47
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 47

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 48

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 49

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 50
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 50

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 51
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 51

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 52

Lys His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 53
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 53

Lys His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 54
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 54

Lys His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 55
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 55

Lys His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 56
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 56

Lys His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 57
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 57

Lys His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 58
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 58

Lys His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 59
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 59

Lys His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 60

Lys His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 61
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 61

Lys His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 62
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 62

Lys His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 63
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 63

Lys His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 64
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 64

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 65
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 65

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 66
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 66

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 67
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 67

Arg His Thr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 68
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 68

Arg His Thr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 69
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 69

Arg His Thr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 70
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 70

Arg His Thr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 71
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 71

Arg His Thr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 72
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 72

Arg His Thr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 73
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 73

Arg His Thr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 74
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 74

Arg His Thr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 75

Arg His Thr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 76

Arg His Thr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 77
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 77

Arg His Thr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 78

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 79
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 79

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 80
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 80

Arg His Phe Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 81
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 81

Arg His Phe Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 82
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 82

Arg His Phe Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 83
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 83

Arg His Phe Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 84
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 84

Arg His Phe Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 85
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 85

Arg His Phe Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 86
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 86

Arg His Phe Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 87
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 87

Arg His Phe Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 88

Arg His Phe Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 89
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 89

Arg His Phe Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 90
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 90

Arg His Phe Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 91
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 91

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 92

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 93
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 93

Arg His Tyr Leu Gln Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 94
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 94

Arg His Tyr Leu Gln Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 95
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 95

Arg His Tyr Leu Gln Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 96
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 96

Arg His Tyr Leu Gln Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 97
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 97

Arg His Tyr Leu Gln Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 98

Arg His Tyr Leu Gln Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 99
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 99

Arg His Tyr Leu Gln Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 100
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 100

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 101

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 101

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 102
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 102

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 103

Arg His Tyr Leu Asn Ile Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 104
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 104

Arg His Tyr Leu Asn Ile Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 105
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 105

Arg His Tyr Leu Asn Ile Val Ser Arg Gln Arg Tyr
1 5 10

<210> 106

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 106

Arg His Tyr Leu Asn Ile Val Thr Lys Gln Arg Tyr
1 5 10

<210> 107
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 107

Arg His Tyr Leu Asn Ile Val Thr Arg Asn Arg Tyr
1 5 10

<210> 108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 108

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Lys Tyr
1 5 10

<210> 109
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 109

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Thr
1 5 10

<210> 110
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 110

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Phe
1 5 10

<210> 111
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 111
Arg His Tyr Leu Asn Val Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 112
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 112

Arg His Tyr Leu Asn Val Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 113
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 113

Arg His Tyr Leu Asn Val Val Ser Arg Gln Arg Tyr
1 5 10

<210> 114
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 114

Arg His Tyr Leu Asn Val Val Thr Lys Gln Arg Tyr
1 5 10

<210> 115
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 115

Arg His Tyr Leu Asn Val Val Thr Arg Asn Arg Tyr
1 5 10

<210> 116
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 116

Arg His Tyr Leu Asn Val Val Thr Arg Gln Lys Tyr
1 5 10

<210> 117
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 117

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Thr
1 5 10

<210> 118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 118

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Phe
1 5 10

<210> 119
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 119

Arg His Tyr Leu Asn Leu Ile Ser Arg Gln Arg Tyr
1 5 10

<210> 120
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 120

Arg His Tyr Leu Asn Leu Ile Thr Lys Gln Arg Tyr
1 5 10

<210> 121
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 121

Arg His Tyr Leu Asn Leu Ile Thr Arg Asn Arg Tyr
1 5 10

<210> 122
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 122

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Lys Tyr
1 5 10

<210> 123
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 123

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Thr
1 5 10

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 124

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Phe
1 5 10

<210> 125
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 125

Arg His Tyr Leu Asn Leu Leu Ser Arg Gln Arg Tyr
1 5 10

<210> 126
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 126

Arg His Tyr Leu Asn Leu Leu Thr Lys Gln Arg Tyr
1 5 10

<210> 127
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 127

Arg His Tyr Leu Asn Leu Leu Thr Arg Asn Arg Tyr
1 5 10

<210> 128
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 128

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Lys Tyr
1 5 10

<210> 129
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 129

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Thr
1 5 10

<210> 130
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 130

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Phe

1 5 10

<210> 131
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 131

Arg His Tyr Leu Asn Leu Val Ser Lys Gln Arg Tyr
1 5 10

<210> 132
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 132

Arg His Tyr Leu Asn Leu Val Ser Arg Asn Arg Tyr
1 5 10

<210> 133
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 133

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Lys Tyr
1 5 10

<210> 134
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 134

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Thr
1 5 10

<210> 135
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 135

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 136
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 136

Arg His Tyr Leu Asn Leu Val Thr Lys Asn Arg Tyr
1 5 10

<210> 137
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 137

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Lys Tyr
1 5 10

<210> 138
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 138

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Thr
1 5 10

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 139

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Phe
1 5 10

<210> 140
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 140

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Lys Tyr
1 5 10

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 141

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Thr
1 5 10

<210> 142
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 142

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Phe
1 5 10

<210> 143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 143

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Thr
1 5 10

<210> 144
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 144

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Phe
1 5 10

<210> 145
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 145

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 146
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 146
Ile Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 147
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 147

Val Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 148
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 148

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 149
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 149

Thr Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 150

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 151

Ser Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 152

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 153
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 153

Thr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 154
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 154

Phe Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 155

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 156

Thr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 157

Phe Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 158
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 158

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 159
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 159

Lys Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 160
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 160

Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 161
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 161

Gln Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 162
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 162

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 163
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 163

Ile Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 164
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 164

Val Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 165
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 165

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 166
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 166

Asp Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 167
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 167

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 168
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 168

Asp Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 169
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 169

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 170
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 170

Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 171
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 171

Thr Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 172

<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 172

Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 173
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 173

Ser Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 174
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 174

Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 175
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 175

Glu Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 176
<211> 27

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 176

Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 177
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 177

Asp Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 178
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 178

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 179
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 179

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 180
<211> 30
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 180

Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 181
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 181

Ser Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 182
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 182

Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 183
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 183

Asp Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 184
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 184

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 185
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 185

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 186
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 186

Arg Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 187
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 187

Gln Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 188
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 188

Asn Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 189
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 189

Leu Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 190
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 190

Val Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 191
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 191

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 192
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 192

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 193

Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 194
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 194

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 195

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 196
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 196

Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 197
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 197

Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 198
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 198

Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 199
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 199

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 200
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 200

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 201
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 201

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 202
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 202

Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 203
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 203

Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 204
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 204

Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 205
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 205

Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 206
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 206

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 207
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 207

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 208
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 208

Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser

1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 209
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 209

Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 210
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 210

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 211
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 211

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 212
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 212

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 213
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 213

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 214

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 215
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 215

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 216
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 216

Pro Ala Glu Asp Leu Ala Gln Tyr Ala Ala Glu Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Leu Thr Arg Gln Arg Tyr
20

<210> 217
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 217

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 218
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 218

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 219
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 219

Ala Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 220
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 220

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 221
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 221

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 222
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nle

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 222

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 223
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ser

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 223

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 224
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 224

Ala Ala Arg Tyr Ser His Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 225
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ile

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 225

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 226
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES

<222> (20)..(20)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 226

Arg Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 227
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 227

Gln Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 228
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 228

Ala Arg Phe Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 229
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> MeLeu

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 229

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 230
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> METHYLATION

<400> 230

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 231
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> desamino

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 231

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 232
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> FORMYLATION

<400> 232

Ala Arg Tyr Tyr Ser Glu Leu Arg Arg Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 233
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nva

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES

<222> (20)..(20)
<223> AMIDATION

<400> 233

Xaa Ala Arg Tyr Ala Ser Ala Leu Arg His Tyr Leu Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 234
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 234

Ala Arg Tyr Tyr Thr Gln Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 235
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> desamino

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 235

Leu Ala Arg Tyr Tyr Ser Asn Leu Arg His Tyr Ile Asn Val Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 236
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 236

Ala Arg Tyr Tyr Asp Ser Leu Arg His Tyr Ile Asn Thr Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 237
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 237

Ala Arg Tyr Tyr Ser Ala Leu Gln His Tyr Ile Asn Leu Leu Thr Arg
1 5 10 15

Pro Arg Tyr

<210> 238
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)

<223> AMIDATION

<400> 238

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg Gln Tyr Arg Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe
20

<210> 239
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 239

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Phe

<210> 240
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 240

Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 241
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 241

Ser Arg Tyr Tyr Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 242
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nle

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 242

Xaa Ala Arg Tyr Tyr Asn Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 243
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D isomer of Ala

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 243

Xaa Arg Tyr Glu Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

His Arg Tyr

<210> 244
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (21)..(21)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Bz

<400> 244

Xaa Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile
1 5 10 15

Thr Arg Pro Arg Phe
20

<210> 245
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 245

Ala Leu Tyr Tyr Ser Ala Leu Arg His Phe Val Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 246
<211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 246

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Val Asn Leu Ile Phe Arg
1 5 10 15

Gln Arg Tyr

<210> 247
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> MeSer

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 247

Xaa Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Met Ile Thr Arg Gln
1 5 10 15

Arg Phe

<210> 248
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>

<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 248

Arg Ile Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe
20

<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminal is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 249

Leu Ser Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 250
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is MeIle

<400> 250

Xaa Arg Tyr Tyr Ser Ala Leu Gln His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 251
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ser

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 251

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Phe

<210> 252
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 252

Met Ala Arg Tyr Tyr Ser Asp Leu Arg Arg Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 253
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>

<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 253

Ala Arg Tyr Tyr Ser Glu Leu Arg His Tyr Ile Ile Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 254
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 254

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 255
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 255

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 256
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> im DNP HIS; 2,2 diphenylalanine Hisitidine

<220>
<221> MOD_RES
<222> (35)..(35)

<223> AMIDATION

<400> 256

Tyr Pro Ala Lys Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu
1 5 10 15

Ser Thr Tyr Tyr Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg
20 25 30

Glx Arg Tyr
35

<210> 257
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 257

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 258
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 258

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 259
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation
<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 259

Ala Ala Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 260
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 260

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 261
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 261

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Xaa Arg Tyr
1 5 10 15

<210> 262
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is p.Cl.Pro; 4 chlorophenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES

<222> (15)..(15)
<223> AMIDATION

<400> 262

Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 263
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 263

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 264
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 264

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 265
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 265

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 266
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> LIPID
<222> (1)..(1)
<223> N alpha myristoyl

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 266

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 267
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N alpha naphthateneacetyl

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 267

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<400> 268

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 269
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 269

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 270
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<220>
<221> MOD_RES
<222> (7)..(7)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 270

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 271
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is 4,4' biphenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<400> 271

Xaa Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 272
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)

<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 272

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 273
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 273

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 274

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 275
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 275

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 276
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<400> 276

Ala Ser Leu Arg Asn Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 277
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is tetrahydroisoquinoline

<400> 277

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 278
<211> 3
<212> PRT
<213> Homo sapiens

<400> 278

000
1

<210> 279
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<400> 279

His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 280
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is 2 thienylalanine

<400> 280

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 281
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 281

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 282
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 282

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 283
<211> 3
<212> PRT
<213> Homo sapiens

<400> 283

000
1

<210> 284
<211> 3
<212> PRT
<213> Homo sapiens

<400> 284

000
1

<210> 285
<211> 3
<212> PRT
<213> Homo sapiens

<400> 285

000
1

<210> 286
<211> 3
<212> PRT
<213> Homo sapiens

<400> 286

000
1

<210> 287
<211> 3
<212> PRT
<213> Homo sapiens

<400> 287

000
1

<210> 288
<211> 3
<212> PRT
<213> Homo sapiens

<400> 288

000
1

<210> 289
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 289

Phe Ser Leu Arg Asn Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 290
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 290

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 291
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 291

Ala Ser Leu Arg His Tyr Trp Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 292
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 292

Ala Ser Leu Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 293
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 293

Ala Ser Leu Arg Ala Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 294
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (14)..(14)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 3' benzothienyalanine

<400> 294

Ala Ser Leu Arg Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 295
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 295

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 296
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 296

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10 15

<210> 297
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is D form of Trp

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N alpha ACETYLATION

<400> 297

Ala Ser Leu Arg His Phe Leu Asn Leu Val Xaa Arg Gln Arg Tyr
1 5 10 15

<210> 298
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 298

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 299
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 299

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 300
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>

<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 300

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 301
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 301

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 302
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE

<222> (10)..(10)
<223> Xaa is Norvaline

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Norleucine

<400> 302

Ala Ser Xaa Arg His Trp Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 303
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 303

Ala Ser Xaa Arg His Trp Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 304
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 304

Ala Ser Xaa Arg His Phe Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 305
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)

<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 305

Ala Ser Xaa Arg His Phe Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 306
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<400> 306

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Xaa Xaa

1 5 10

<210> 307
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 307

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10

<210> 308
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 308

Ala Ser Leu Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 309
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 309

Ala Ser Xaa Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> bonded to OCH3

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 310

Ile Asn Pro Ile Tyr Arg Leu Arg Tyr
1 5

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (4)..(4)
<223> Sequence is linked to identical sequence by a disulfide bond

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> C terminus is bonded to NH2

<400> 311

Ile Asn Pro Cys Tyr Arg Leu Arg Tyr
1 5

<210> 312
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> C terminus is bonded to OCH3

<220>
<221> DISULFID
<222> (1)..(1)
<223> sequence is linked to an identical sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 312

Cys Tyr Arg Leu Arg Tyr
1 5

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Connected by NH CH CO

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Identical peptide chains are connected by (CH2)4 at the CH o
f NH CH CO

<400> 313

Ile Asn Pro Tyr Arg Leu Arg Tyr
1 5

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> C terminus is bonded to OCH3

<400> 314

Tyr Arg Leu Arg Tyr Tyr Arg Leu Arg Tyr
1 5 10

<210> 315
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (18)..(22)
<223>

<400> 315

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala
1 5 10 15

Arg Cys Tyr Ser Ala Cys Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
20 25 30

Arg Tyr

<210> 316
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 316

Arg His Tyr Leu Asn Leu Ile Gly Arg Gln Arg Tyr
1 5 10

<210> 317
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (3)..(7)
<223> ACETYLATION

<400> 317

Arg His Gly Leu Asn Leu Leu Gly Arg Gln Arg Tyr
1 5 10

<210> 318
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 318

Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 319
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 319

His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 320
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 320

Arg His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 321
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 321

Tyr Ile Asn Leu Leu Tyr Arg Gln Arg Tyr
1 5 10

<210> 322
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 6 amino hexanoic acid

<400> 322

Tyr Pro Ser Leu Xaa Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10 15

<210> 323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 323

Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5

<210> 324
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 324

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 325
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 325

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 326
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminal is bonded to H

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 326

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 327
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>

<221> MOD_RES
<222> (9)..(9)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 327

Ala Ser Leu Arg Thr Arg Gln Arg Tyr
1 5

<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 328

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 329
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 329

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 330

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 330

Asp Asp Asp Asp Tyr
1 5

<210> 331
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 331

Gly Pro Arg
1

<210> 332
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 332

Ala Gly Gly
1

<210> 333
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 333

His Pro Phe His Leu
1 5

<210> 334
<211> 34
<212> PRT
<213> Homo sapiens

<400> 334

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 335
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 335

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala
1 5 10 15

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
20 25 30

Arg Tyr

<210> 336
<211> 37
<212> PRT
<213> Homo sapiens

<400> 336

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe The Ser Asp Val
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

Val Lys Gly Arg Gly
35

<210> 337
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> C terminus is bonded to NH2

<400> 337

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe The Ser Asp Val
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

Val Lys Gly Arg
35

<210> 338
<211> 31
<212> PRT
<213> Homo sapiens

<400> 338

His Ala Glu Gly Thr Phe The Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

<210> 339
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> C terminus is bonded to NH2

<400> 339

His Ala Glu Gly Thr Phe The Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
20 25 30

<210> 340
<211> 37
<212> PRT
<213> Homo sapiens

<400> 340

His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser
1 5 10 15

Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asp Thr Lys Arg Asn
20 25 30

Lys Asn Asn Ile Ala
35

<210> 341

<211> 463

<212> PRT

<213> homo sapiens

<400> 341

Met Ala Gly Ala Pro Gly Pro Leu Arg Leu Ala Leu Leu Leu Leu Gly
1 5 10 15

Met Val Gly Arg Ala Gly Pro Arg Pro Gln Gly Ala Thr Val Ser Leu
20 25 30

Trp Glu Thr Val Gln Lys Trp Arg Glu Tyr Arg Arg Gln Cys Gln Arg
35 40 45

Ser Leu Thr Glu Asp Pro Pro Pro Ala Thr Asp Leu Phe Cys Asn Arg
50 55 60

Thr Phe Asp Glu Tyr Ala Cys Trp Pro Asp Gly Glu Pro Gly Ser Phe
65 70 75 80

Val Asn Val Ser Cys Pro Trp Tyr Leu Pro Trp Ala Ser Ser Val Pro
85 90 95

Gln Gly His Val Tyr Arg Phe Cys Thr Ala Glu Gly Leu Trp Leu Gln
100 105 110

Lys Asp Asn Ser Ser Leu Pro Trp Arg Asp Leu Ser Glu Cys Glu Glu
115 120 125

Ser Lys Arg Gly Glu Arg Ser Ser Pro Glu Glu Gln Leu Leu Phe Leu
130 135 140

Tyr Ile Ile Tyr Thr Val Gly Tyr Ala Leu Ser Phe Ser Ala Leu Val
145 150 155 160

Ile Ala Ser Ala Ile Leu Leu Gly Phe Arg His Leu His Cys Thr Arg
165 170 175

Asn Tyr Ile His Leu Asn Leu Phe Ala Ser Phe Ile Leu Arg Ala Leu
180 185 190

Ser Val Phe Ile Lys Asp Ala Ala Leu Lys Trp Met Tyr Ser Thr Ala
195 200 205

Ala Gln Gln His Gln Trp Asp Gly Leu Leu Ser Tyr Gln Asp Ser Leu
210 215 220

Ser Cys Arg Leu Val Phe Leu Leu Met Gln Tyr Cys Val Ala Ala Asn
225 230 235 240

Tyr Tyr Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Thr Leu Leu Ala
245 250 255

Phe Ser Val Phe Ser Glu Gln Trp Ile Phe Arg Leu Tyr Val Ser Ile
260 265 270

Gly Trp Gly Val Pro Leu Leu Phe Val Val Pro Trp Gly Ile Val Lys
275 280 285

Tyr Leu Tyr Glu Asp Glu Gly Cys Trp Thr Arg Asn Ser Asn Met Asn
290 295 300

Tyr Trp Leu Ile Ile Arg Leu Pro Ile Leu Phe Ala Ile Gly Val Asn
305 310 315 320

Phe Leu Ile Phe Val Arg Val Ile Cys Ile Val Val Ser Lys Leu Lys
325 330 335

Ala Asn Leu Met Cys Lys Thr Asp Ile Lys Cys Arg Leu Ala Lys Ser
340 345 350

Thr Leu Thr Leu Ile Pro Leu Leu Gly Thr His Glu Val Ile Phe Ala
355 360 365

Phe Val Met Asp Glu His Ala Arg Gly Thr Leu Arg Phe Ile Lys Leu
370 375 380

Phe Thr Glu Leu Ser Phe Thr Ser Phe Gln Gly Leu Met Val Ala Ile
385 390 395 400

Leu Tyr Cys Phe Val Asn Asn Glu Val Gln Leu Glu Phe Arg Lys Ser
405 410 415

Trp Glu Arg Trp Arg Leu Glu His Leu His Ile Gln Arg Asp Ser Ser
420 425 430

Met Lys Pro Leu Lys Cys Pro Thr Ser Ser Leu Ser Ser Gly Ala Thr
435 440 445

Ala Gly Ser Ser Met Tyr Thr Ala Thr Cys Gln Ala Ser Cys Ser
450 455 460

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
17 July 2003 (17.07.2003)

PCT

(10) International Publication Number
WO 03/057235 A3

(51) International Patent Classification[7]: A61K 38/17, 38/26, A61P 3/04

(21) International Application Number: PCT/GB03/00062

(22) International Filing Date: 10 January 2003 (10.01.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

0200507.2	10 January 2002 (10.01.2002)	GB
60/392,109	28 June 2002 (28.06.2002)	US
PCT/US02/31944	24 September 2002 (24.09.2002)	US

(71) Applicants *(for all designated States except US)*: **IMPERIAL COLLEGE INNOVATIONS LTD** [GB/GB]; 47 Prince's Gate, Exhibition Road, London SW7 2QA (GB). **OREGON HEALTH AND SCIENCE UNIVERSITY** [US/US]; 2525 S.W. First Avenue, Suite AD-120, Portland, OR 97201 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **COWLEY, Michael** [AU/US]; 6724 S.E. 19th Avenue, Portland, OR 97202 (US). **CONE, Roger** [US/US]; 16563 S. Hattan Road, Oregon City, OR 97045 (US). **LOW, Malcolm** [NZ/US]; 4650 S.W. Upper Drive, Lake Oswego, OR 97035 (US). **BUTLER, Andrew** [NZ/US]; 3730 S.W. 12th Avenue, Apartment 10, Portland, OR 97201 (US). **BLOOM, Stephen, Robert** [GB/GB]; Imperial College Innovations Limited, 47 Prince's Gate, Exhibition Road, London SW7 2QA (GB). **SMALL, Caroline, Jane** [GB/GB]; Imperial College Innovations Limited, 47 Prince's Gate, Exhibition Road, London SW7 2QA (GB). **BATTERHAM, Rachel, Louise** [GB/GB]; Imperial College Innovations Limited, 47 Prince's Gate, Exhibition Road, London SW7 2QA (GB). **GHATEI, Mohammad, Ali** [GB/GB]; Imperial College Innovations Limited, 47 Prince's Gate, Exhibition Road, London SW7 2QA (GB).

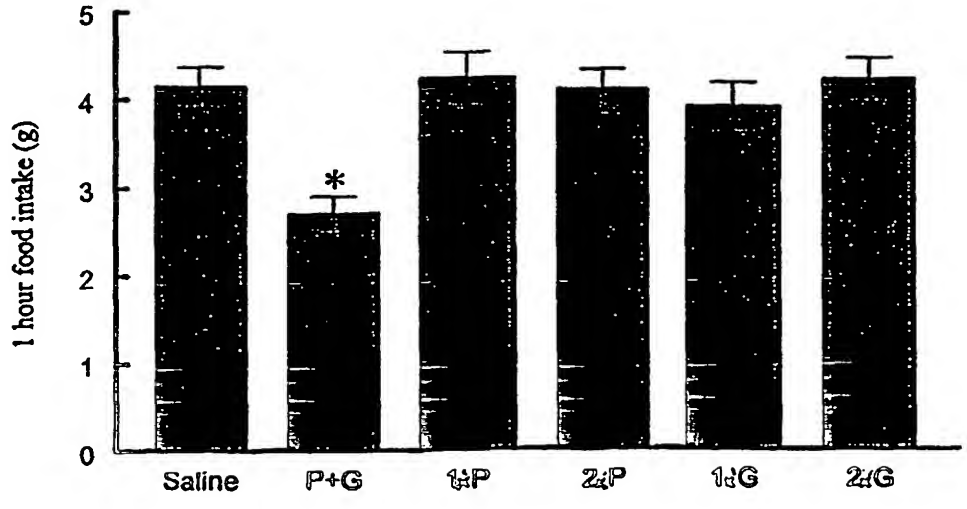
(74) Agents: **SILVESTON, Judith** et al.; Abel & Imray, 20 Red Lion Street, London WC1R 4PQ (GB).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),

[Continued on next page]

(54) Title: MODIFICATION OF FEEDING BEHAVIOR



(57) Abstract: Methods are disclosed for decreasing calorie intake, food intake, and appetite in a subject. The methods include peripherally administering PYY or an agonist thereof and GLP-1 or an agonist thereof to the subject, simultaneously or sequentially, thereby decreasing the calorie intake of the subject.

WO 03/057235 A3

Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report:
11 December 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

PCT/GB 03/00062

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 A61K38/17 A61K38/26 A61P3/04

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

WPI Data, EPO-Internal, PAJ, BIOSIS, EMBASE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00 47219 A (LU HUANG HUI ;ONTOGENY INC (US); PANG KEVIN (US)) 17 August 2000 (2000-08-17) claims page 34, line 3 - line 12	1-57
A	US 6 191 102 B1 (EFENDIC SUAD ET AL) 20 February 2001 (2001-02-20) claims	1-57
A	WO 01 51078 A (AMYLIN PHARMACEUTICALS INC) 19 July 2001 (2001-07-19) claims	1-57

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
10 September 2003	19/09/2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Böhmerova, E

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
A	ROSSI M ET AL: "Central nervous system neuropeptides involved in obesity." HANDBOOK OF EXPERIMENTAL PHARMACOLOGY, vol. 149, 2000, pages 313-341, XP001154661 2000 Springer-Verlag GmbH & Co. KG;Springer-Verlag New York Inc. Heidelberger Platz 3, D-14197, Berlin, Germany; 175 Fifth Avenue, New York, NY, 10010-7858, USA ISSN: 0171-2004 the whole document	1-57
A	CLAPHAM J C ET AL: "ANTI-OBESITY DRUGS: A CRITICAL REVIEW OF CURRENT THERAPIES AND FUTURE OPPORTUNITIES" PHARMACOLOGY AND THERAPEUTICS, ELSEVIER, GB, vol. 89, no. 1, 2001, pages 81-121, XP001120530 ISSN: 0163-7258 the whole document	1-57
P,X	WO 02 47712 A (PITTNER RICHARD A ;YOUNG ANDREW A (US); AMYLIN PHARMACEUTICALS INC) 20 June 2002 (2002-06-20) claims page 6, line 25 -page 8, line 4	1-57

INTERNATIONAL SEARCH REPORT

PCT/GB 03/00062

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 1 - 33 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/GB 03/00062

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 0047219	A	17-08-2000	AU	3486800 A	29-08-2000
			CA	2360324 A1	17-08-2000
			EP	1189629 A2	27-03-2002
			JP	2003518914 T	17-06-2003
			WO	0047219 A2	17-08-2000
US 6191102	B1	20-02-2001	AT	234112 T	15-03-2003
			AU	734042 B2	31-05-2001
			AU	5245798 A	29-05-1998
			DE	69719798 D1	17-04-2003
			DK	946191 T3	14-07-2003
			EP	1306092 A2	02-05-2003
			EP	0946191 A1	06-10-1999
			HU	0003314 A2	28-02-2001
			NO	992557 A	15-06-1999
			NZ	335995 A	23-02-2001
			PL	334317 A1	14-02-2000
			PT	946191 T	30-06-2003
			WO	9819698 A1	14-05-1998
			US	6583111 B1	24-06-2003
			ZA	9709904 A	25-05-1998
WO 0151078	A	19-07-2001	AU	2413600 A	01-08-2000
			AU	2638001 A	24-07-2001
			AU	3581900 A	01-08-2000
			BR	0007820 A	20-11-2001
			BR	0007823 A	20-11-2001
			CA	2356331 A1	20-07-2000
			CA	2356706 A1	20-07-2000
			CA	2396157 A1	19-07-2001
			CN	1384755 T	11-12-2002
			CN	1347327 T	01-05-2002
			EP	1143989 A2	17-10-2001
			EP	1140145 A2	10-10-2001
			EP	1246638 A1	09-10-2002
			JP	2002534450 T	15-10-2002
			JP	2002538084 T	12-11-2002
			JP	2003519667 T	24-06-2003
			NO	20013468 A	14-09-2001
			NO	20013469 A	14-09-2001
			WO	0041546 A2	20-07-2000
			WO	0041548 A2	20-07-2000
			WO	0151078 A1	19-07-2001
			US	2003087820 A1	08-05-2003
			US	2003036504 A1	20-02-2003
WO 0247712	A	20-06-2002	AU	3084302 A	24-06-2002
			WO	0247712 A2	20-06-2002
			US	2002141985 A1	03-10-2002